

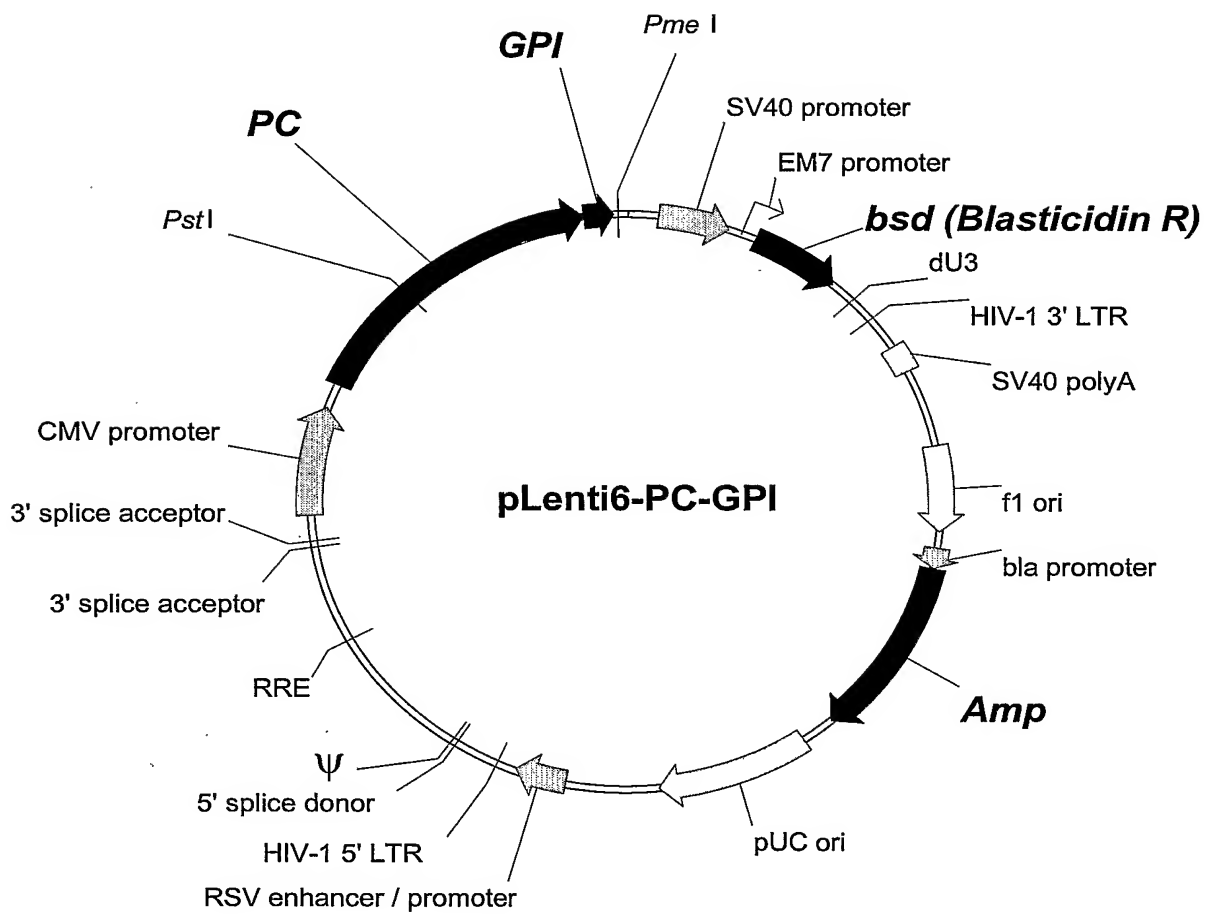
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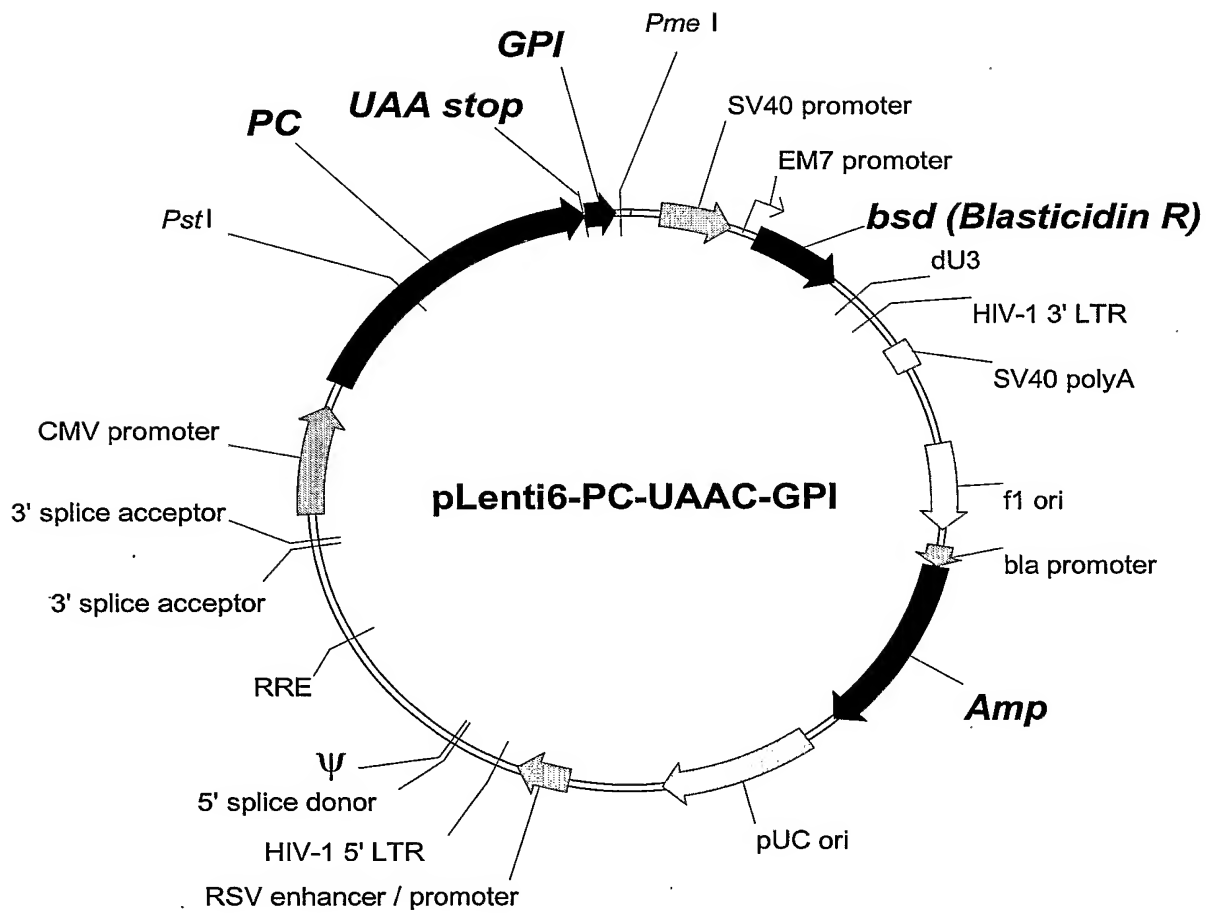
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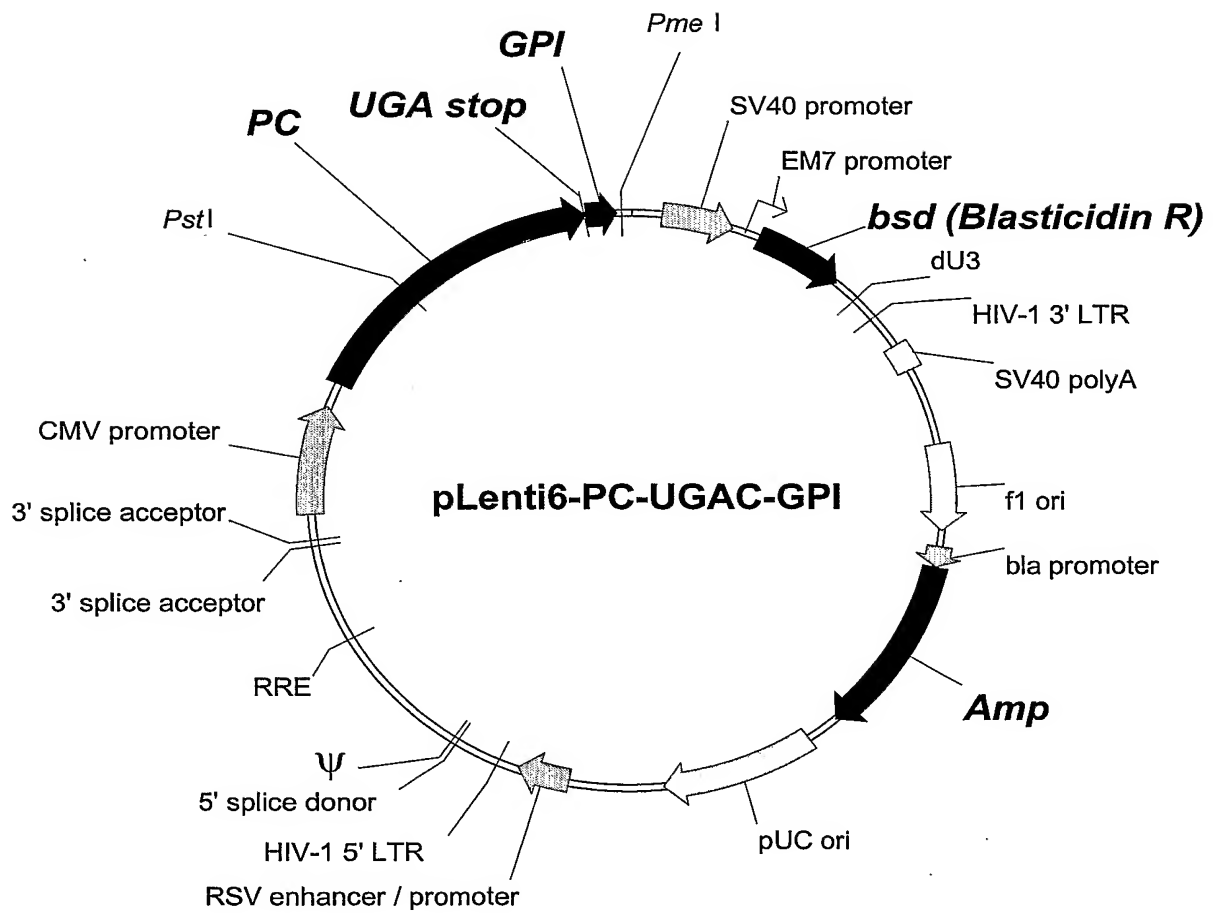
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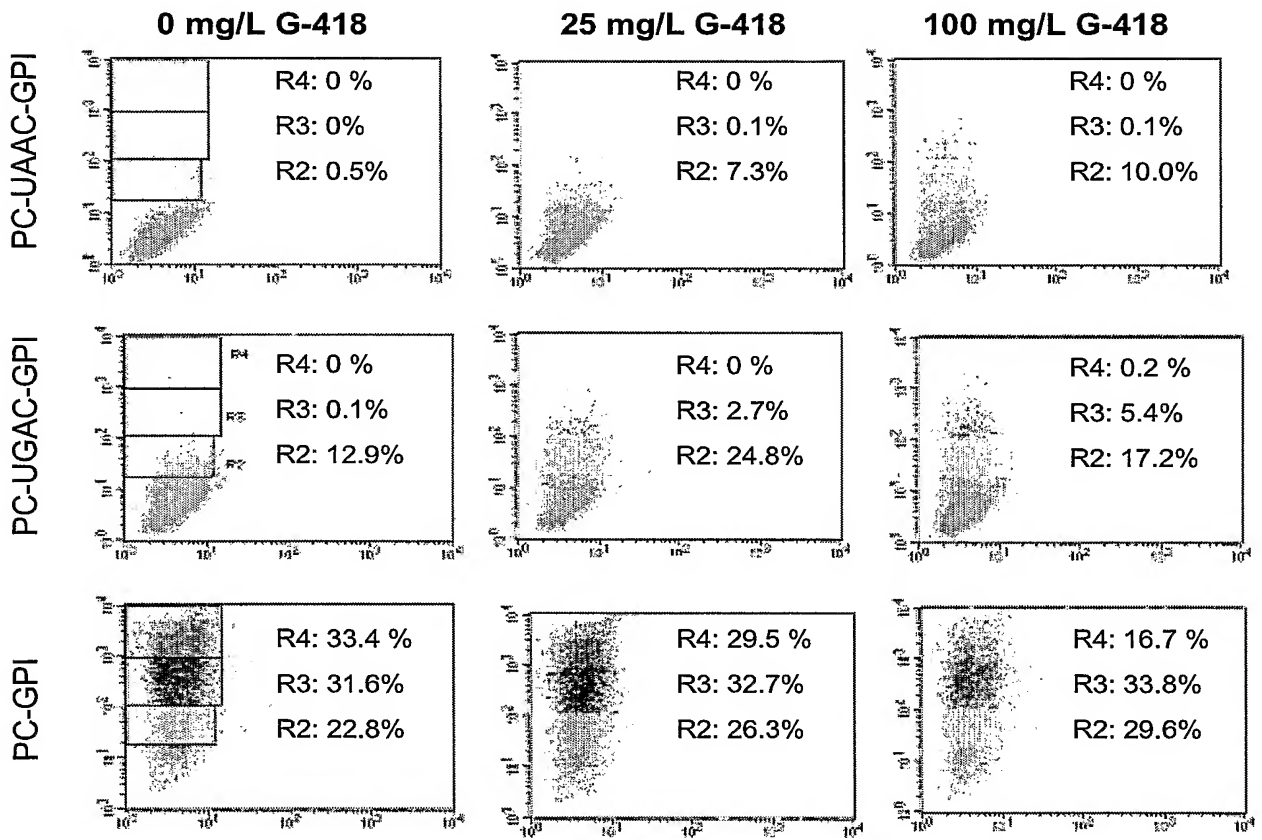
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Figure 5

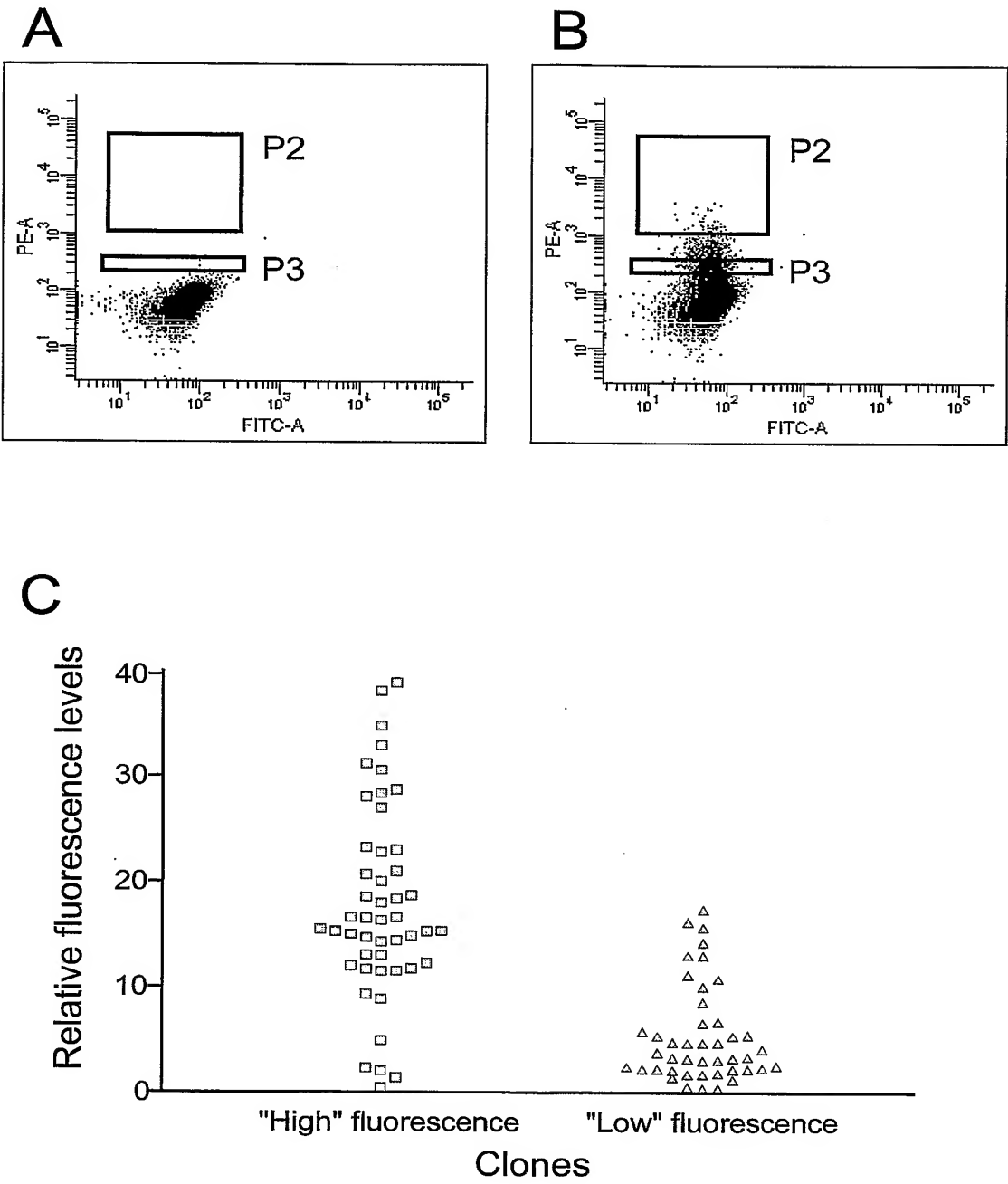
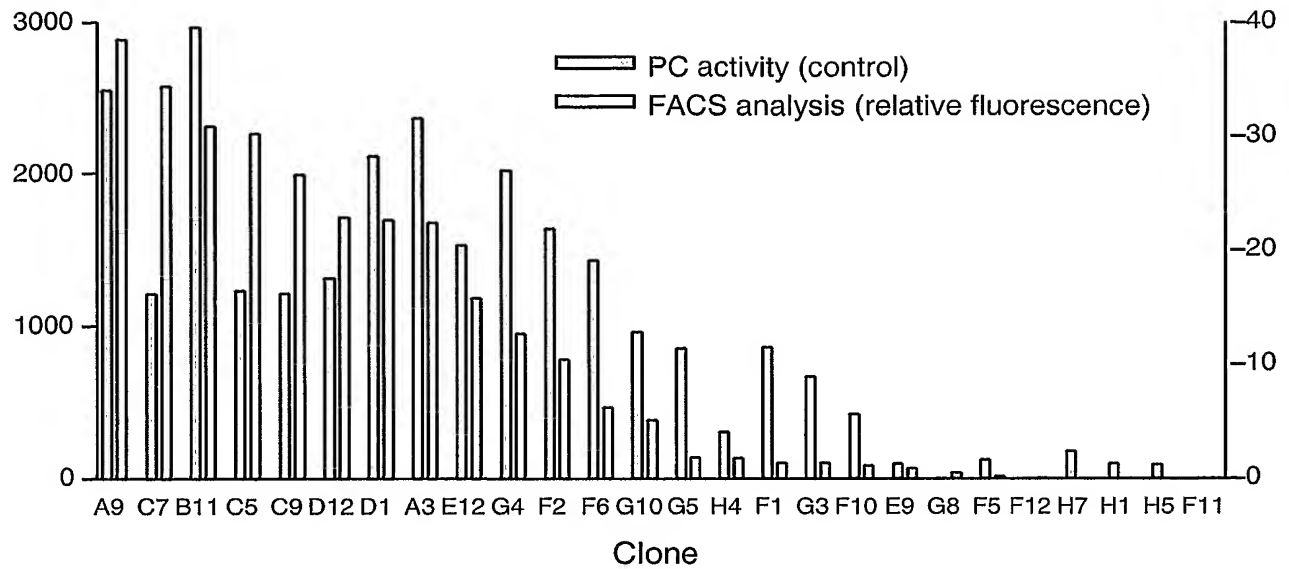


Figure 6**A**

Left axis: Soluble PC activity (ng/mL) Right axis: Relative fluorescence

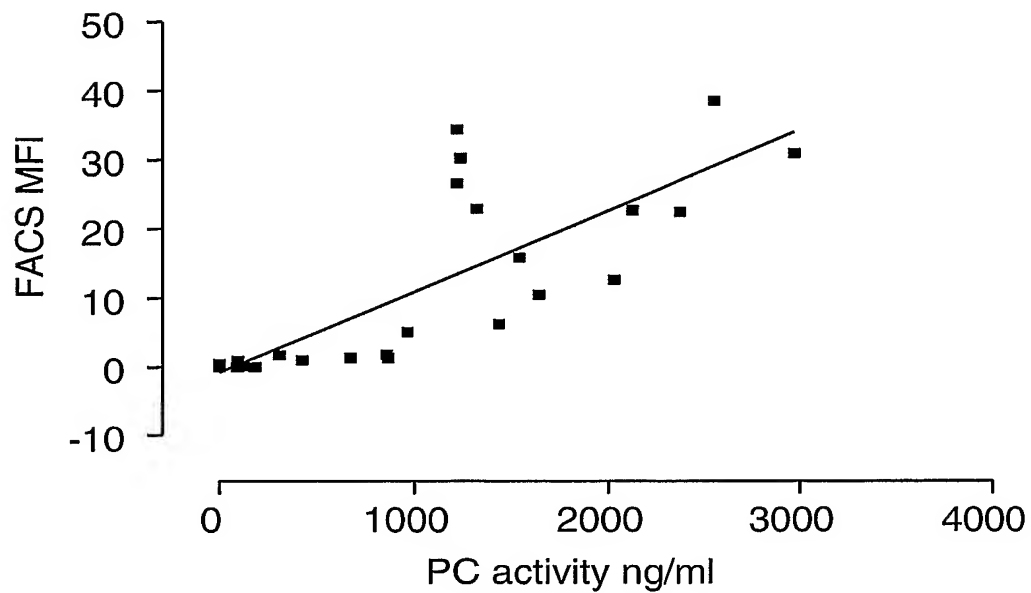
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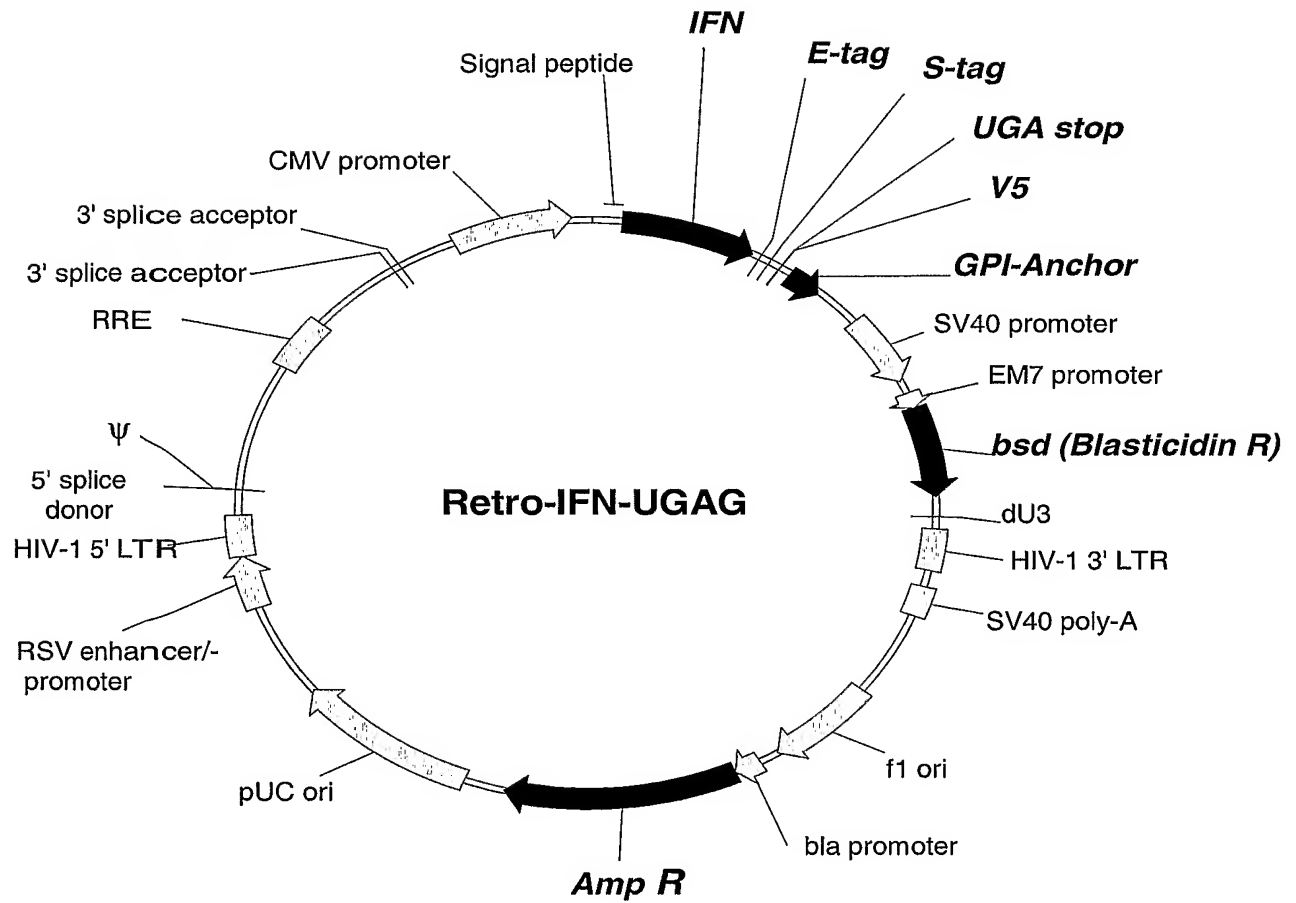
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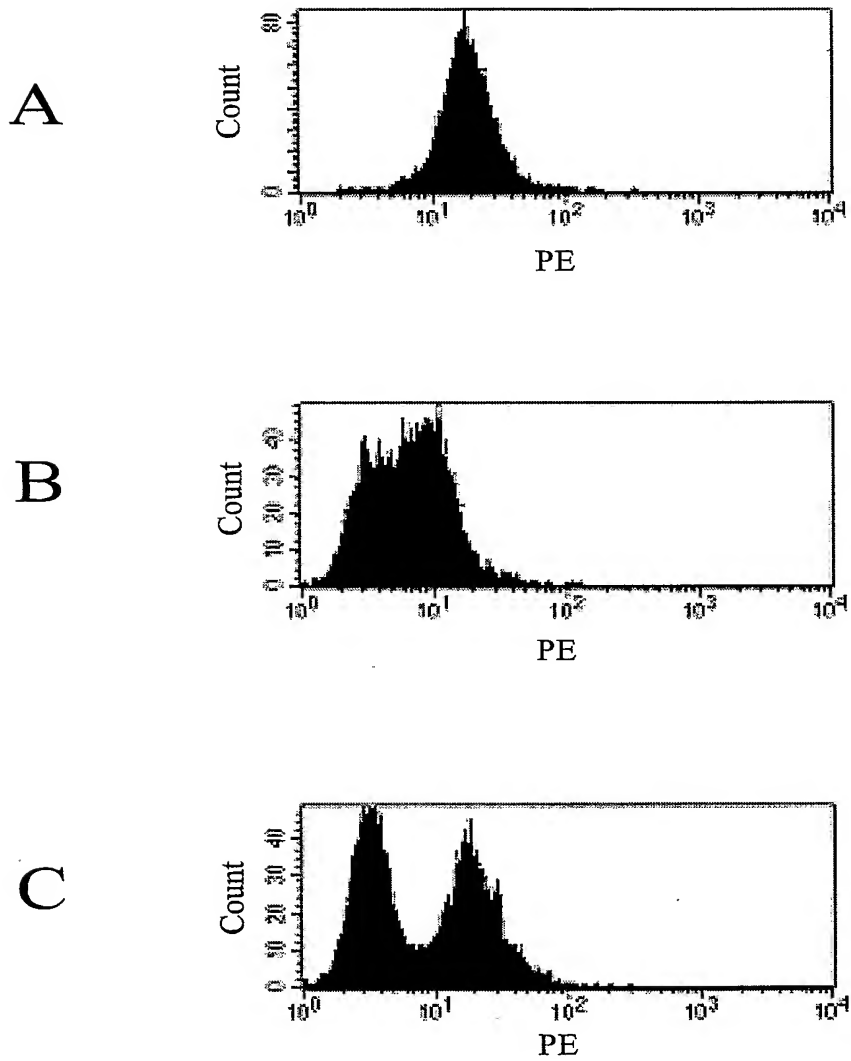
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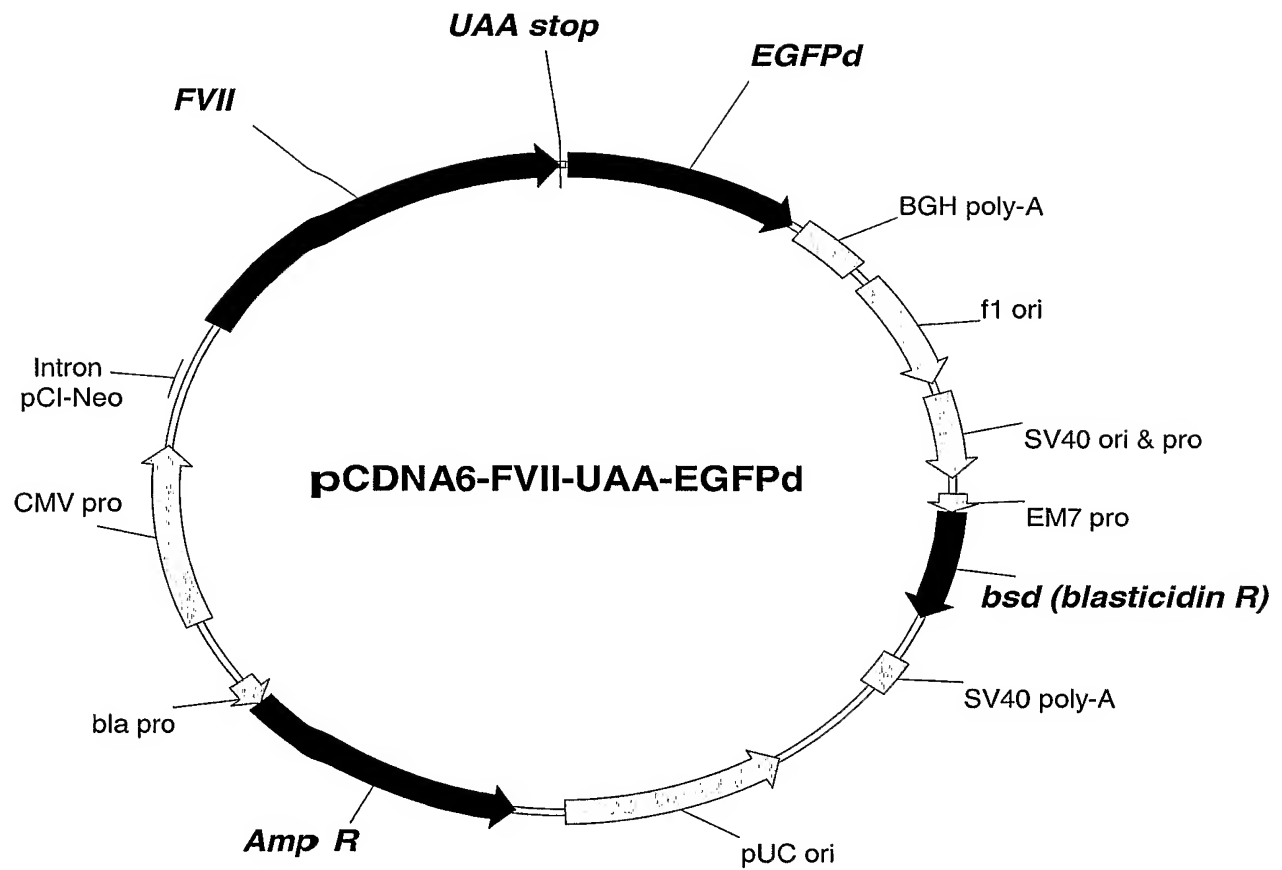
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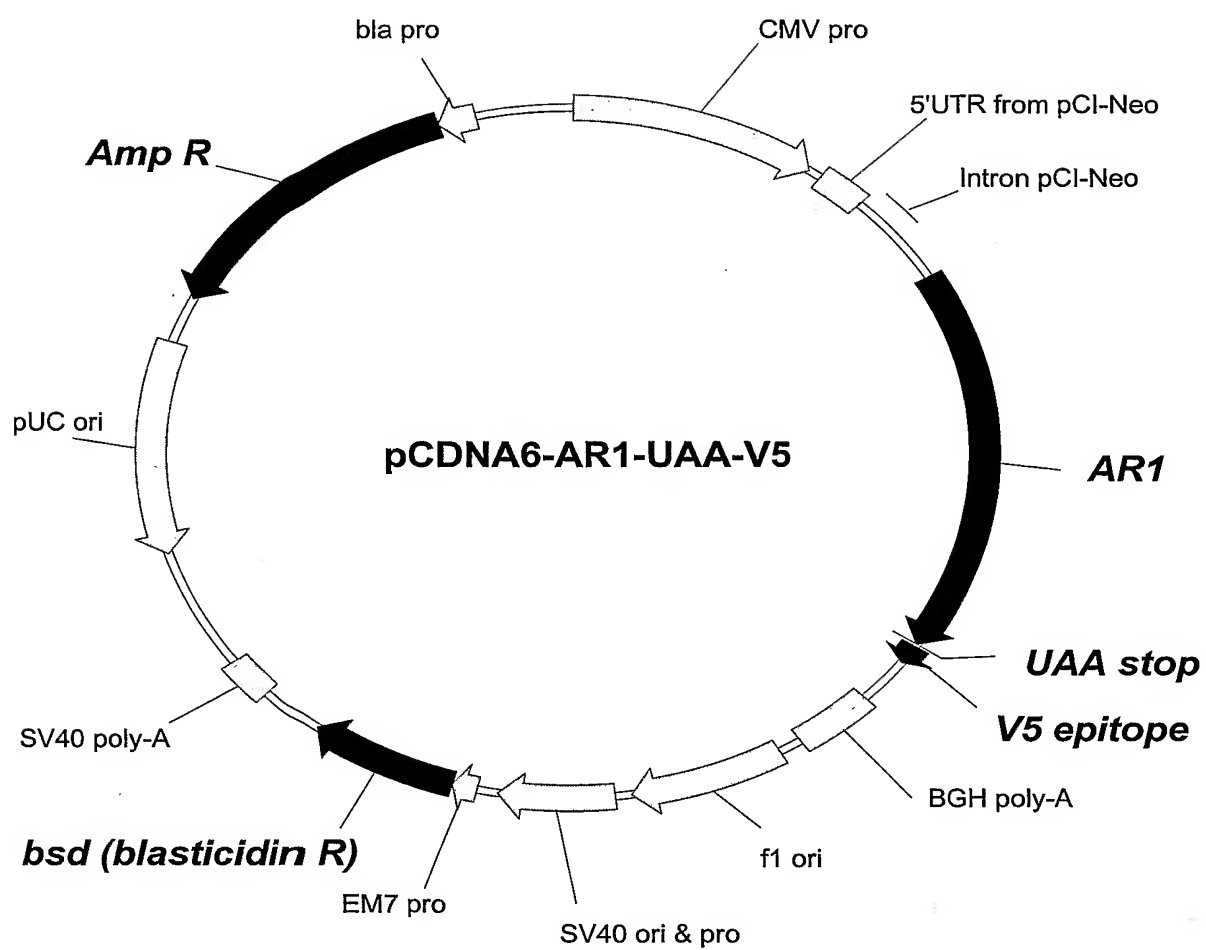
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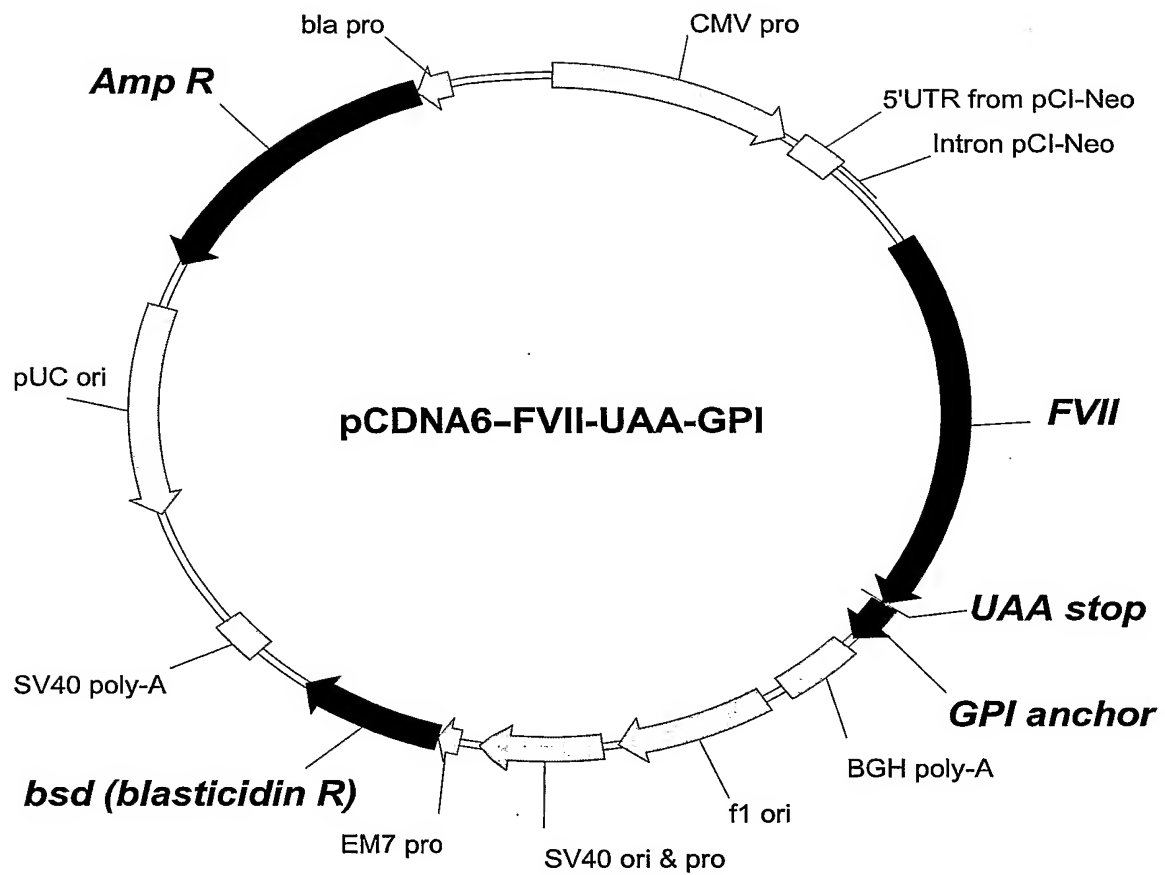
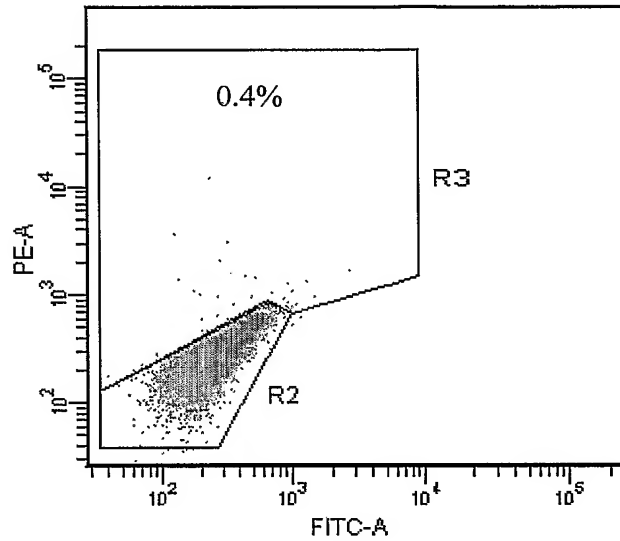
Figure 11

Figure 12

A) Negative CHO-K1 control



B) Transfected CHO-K1 cells

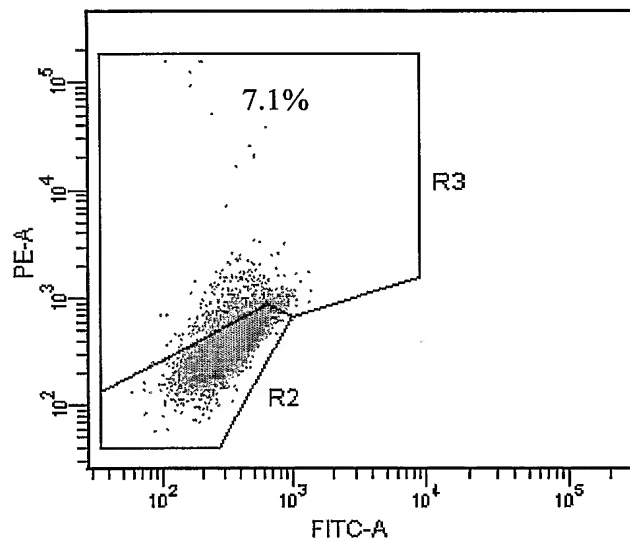
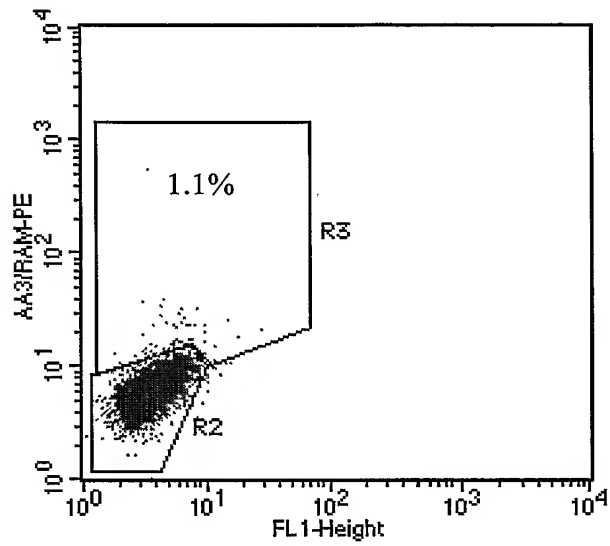


Figure 13

A) Negative CHO-K1 control



B) Transfected CHO-K1 cells

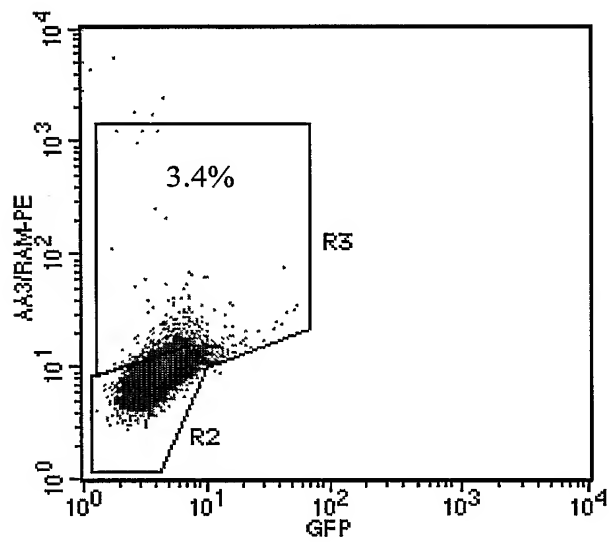


Figure 14 (PC-GPI)

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      M W Q L T S L L L F V A T W G I S G T P
1  ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTTT CGGCACACCA
      A P L D S V F S S S E R A H Q V L R I R
61  GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
      K R A N S F L E E L R H S S L E R E C I
121 AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
      E E I C D F E E A K E I F Q N V D D T L
181 GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACACTG
      A F W S K H V D G D Q C L V L P L E H P
241 GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
      C A S L C C G H G T C I D G I G S F S C
301 TGCGCCAGCC TGTGCTGCGG GCACGGCACG TGCATCGACG GCATCGGCAG CTTCAGCTGC
      D C R S G W E G R F C Q R E V S F L N C
361 GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
      S L D N G G C T H Y C L E E V G W R R C
421 TCGTTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
      S C A P G Y K L G D D L L Q C H P A V K
481 AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTACACC CGCAGTGAAG
      F P C G R P W K R M E K K R S H L K R D
541 TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
      T E D Q E D Q V D P R L I D G K M T R R
601 ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
      G D S P W Q V V L L D S K K K L A C G A
661 GGAGACAGCC CCTGGCAGGT GGTCTGTCTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
      V L I H P S W V L T A A A H C M D E S K K
721 GTGCTCATCT ACCCCTCCTG GGTGTGTGAC GCGGCCCACT GCATGGATGA GTCCAAGAAG
      L L V R L G E Y D L R R W E K W E L D L
781 CTCCTTGTCA GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
      D I K E V F V H P N Y S K S T T D N D I
841 GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
      A L L H L A Q P A T L S Q T I V P I C L
901 GCACTGCTGC ACCTGGCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCTC
      P D S G L A E R E L N Q A G Q E T L V T
961 CCGGACAGCG GCCTTGCA GA GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
      G W G Y H S S R E K E A K R N R T F V L
1021 GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCGTCCTC
      N F I K I P V V P H N E C S E V M S N M
1081 AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
      V S E N M L C A G I L G D R Q D A C E G
1141 GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
      D S G G P M V A S F H G T W F L V G L V
1201 GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GTTTCCTGGT GGGCCTGGTG
      S W G E G C G L L H N Y G V Y T K V S R
1261 AGCTGGGGTG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
      Y L D W I H G H I R D K E A P Q K S W A
1321 TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCAGAA GAGCTGGGCA
      P L E P T Y C D L A P P A G T T D A A H
1381 CCTCTGGAAC CCACGTACTG CGACCTCGCC CCTCCCGCTG GCACGACCGA TGCCGCTCAC
      P G R S V V P A L L P L L A G T L L L L
1441 CCTGGCCGGA GCGTCGTGCC TGCCCTCCTG CCTCTGCTCG CCGGGACCCT CCTGCTCCTG
      E T A T A P *
1501 GAAACCGCTA CCGCTCCCTA GTAA

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Figure 15 (PC-UAAC-GPI)

```

      M W Q L T S L L L F V A T W G I S G T P
1  ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTC CGGCACACCA
      A P L D S V F S S S E R A H Q V L R I R
61  GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
      K R A N S F L E E L R H S S L E R E C I
121 AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
      E E I C D F E E A K E I F Q N V D D T L
181 GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACTCTG
      A F W S K H V D G D Q C L V L P L E H P
241 GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
      C A S L C C G H G T C I D G I G S F S C
301 TGCGCCAGCC TGTGCTGCGG GCACGGCAGC TGCATCGACG GCATCGGCAG CTTCAGCTGC
      D C R S G W E G R F C Q R E V S F L N C
361 GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
      S L D N G G C T H Y C L E E V G W R R C
421 TCGTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
      S C A P G Y K L G D D L L Q C H P A V K
481 AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTACCC CGCAGTGAAG
      F P C G R P W K R M E K K R S H L K R D
541 TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
      T E D Q E D Q V D P R L I D G K M T R R
601 ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
      G D S P W Q V V L L D S K K K L A C G A
661 GGAGACAGCC CCTGGCAGGT GGTCTGCTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
      V L I H P S W V L T A A A H C M D E S K K
721 GTGCTCATCT ACCCTCCTG GGTGCTGACA GCGGCCCACT GCATGGATGA GTCCAAGAAG
      L L V R L G E Y D L R R W E K W E L D L
781 CTCCTTGTC A GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
      D I K E V F V H P N Y S K S T T D N D I
841 GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
      A L L H L A Q P A T L S Q T I V P I C L
901 GCACTGCTGC ACCTGGCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCCTC
      P D S G L A E R E L N Q A G Q E T L V T
961 CCGGACAGCG GCCTTGCA GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
      G W G Y H S S R E K E A K R N R T F V L
1021 GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCGTCCTC
      N F I K I P V V P H N E C S E V M S N M
1081 AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
      V S E N M L C A G I L G D R Q D A C E G
1141 GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
      D S G G P M V A S F H G T W F L V G L V
1201 GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GGTTCCTGGT GGGCCTGGTG
      S W G E G C G L L H N Y G V Y T K V S R
1261 AGTGCGGGG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
      Y L D W I H G H I R D K E A P Q K S W A
1321 TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCAGAA GAGCTGGGCA
      P * L E P T Y C D L A P P A G T T D A A
1381 CCTTAACTGG AACCCACGTA CTGCGACCTC GCCCTCCCG CTGGCAGGAC CGATGCCGCT
      H P G R S V V P A L L P L L A G T L L L
1441 CACCCTGGCC GGAGCGTCGT GCCTGCCCTC CTGCCTCTGC TCGCCGGGAC CCTCCTGCTC
      L E T A T A P * * * *
1501 CTGGAAACCG CTACCGCTCC CTAGTAATAG TGA

```

Figure 16 (PC-UGAC-GPI)

```

      M W Q L T S L L L F V A T W G I S G T P
1  ATGTGGCAGC TCACAAGCCT CCTGCTGTTC GTGGCCACCT GGGGAATTTC CGGCACACCA
      A P L D S V F S S S E R A H Q V L R I R
61  GCTCCTCTTG ACTCAGTGTT CTCCAGCAGC GAGCGTGCCC ACCAGGTGCT GCGCATCCGC
      K R A N S F L E E L R H S S L E R E C I
121 AAACGTGCCA ACTCCTTCCT GGAGGAGCTC CGTCACAGCA GCCTGGAGCG GGAGTGCATA
      E E I C D F E E A K E I F Q N V D D T L
181 GAGGAGATCT GTGACTTCGA GGAGGCCAAG GAAATTTTCC AAAATGTGGA TGACACTG
      A F W S K H V D G D Q C L V L P L E H P
241 GCCTTCTGGT CCAAGCACGT CGACGGTGAC CAGTGCTTGG TCTTGCCCTT GGAGCACCCG
      C A S L C C G H G T C I D G I G S F S C
301 TCGCCAGCC TGTGCTGCGG GCACGGCACG TGCATCGACG GCATCGGCAG CTTCAGCTGC
      D C R S G W E G R F C Q R E V S F L N C
361 GACTGCCGCA GCGGCTGGGA GGGCCGCTTC TGCCAGCGCG AGGTGAGCTT CCTCAATTGC
      S L D N G G C T H Y C L E E V G W R R C
421 TCGTGGACA ACGGCGGCTG CACGCATTAC TGCCTAGAGG AGGTGGGCTG GCGGCGCTGT
      S C A P G Y K L G D D L L Q C H P A V K
481 AGCTGTGCGC CTGGCTACAA GCTGGGGGAC GACCTCCTGC AGTGTACCC CGCAGTGAAG
      F P C G R P W K R M E K K R S H L K R D
541 TTCCCTTGTG GGAGGCCCTG GAAGCGGATG GAGAAGAAGC GCAGTCACCT GAAACGAGAC
      T E D Q E D Q V D P R L I D G K M T R R
601 ACAGAAGACC AAGAAGACCA AGTAGATCCG CGGCTCATTG ATGGGAAGAT GACCAGGCGG
      G D S P W Q V V L L D S K K K L A C G A
661 GGAGACAGCC CCTGGCAGGT GGTCTCTGTG GACTCAAAGA AGAAGCTGGC CTGCGGGGCA
      V L I H P S W V L T A A A H C M D E S K K
721 GTGCTCATCC ACCCTCCTG GGTGCTGACA GCGGCCCACT GCATGGATGA GTCCAAGAAG
      L L V R L G E Y D L R R W E K W E L D L
781 CTCCTTGTC A GGCTTGGAGA GTATGACCTG CGGCGCTGGG AGAAGTGGGA GCTGGACCTG
      D I K E V F V H P N Y S K S T T D N D I
841 GACATCAAGG AGGTCTTCGT CCACCCCAAC TACAGCAAGA GCACCACCGA CAATGACATC
      A L L H L A Q P A T L S Q T I V P I C L
901 GCACTGCTGC ACCTGGCCCCA GCCCGCCACC CTCTCGCAGA CCATAGTGCC CATCTGCCTC
      P D S G L A E R E L N Q A G Q E T L V T
961 CCGGACAGCG GCCTTGCA A GCGCGAGCTC AATCAGGCCG GCCAGGAGAC CCTCGTGACG
      G W G Y H S S R E K E A K R N R T F V L
1021 GGCTGGGGAT ATCACAGCAG CCGAGAGAAG GAGGCCAAGA GAAACCGCAC CTTCTGTCCTC
      N F I K I P V V P H N E C S E V M S N M
1081 AACTTCATCA AGATTCCCGT GGTCCCGCAC AATGAGTGCA GCGAGGTCAT GAGCAACATG
      V S E N M L C A G I L G D R Q D A C E G
1141 GTGTCTGAGA ACATGCTGTG TGCGGGCATC CTCGGGGACC GGCAGGATGC CTGCGAGGGC
      D S G G P M V A S F H G T W F L V G L V
1201 GACAGTGGGG GGCCCATGGT CGCCTCCTTC CACGGCACCT GGTTCCTGGT GGGCCTGGTG
      S W G E G C G L L H N Y G V Y T K V S R
1261 AGTGGGGTG AGGGCTGTGG GCTCCTTCAC AACTACGGCG TTTACACCAA AGTCAGCCGC
      Y L D W I H G H I R D K E A P Q K S W A
1321 TACCTCGACT GGATTCATGG GCACATCAGA GACAAGGAAG CCCCCAGAA GAGCTGGGCA
      P * L E P T Y C D L A P P A G T T D A A
1381 CCTTGACTGG AACCACGTA CTGCGACCTC GCCCTCCCG CTGGCAGCAC CGATGCCGCT
      H P G R S V V P A L L P L L A G T L L L
1441 CACCTGGCC GGAGCGTCGT GCCTGCCCTC CTGCCTCTGC TCGCCGGGAC CCTCCTGCTC
      L E T A T A P * * * *
1501 CTGGAAACCG CTACCGCTCC CTAGTAATAG TGA

```


Figure 17 (FVII-UAA-GPI)

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      M V S Q A L R L L C L L L G L Q G C L A
1  ATGGTCAGCC AGGCCCTCCG CCTCCTGTGC CTGCTCCTGG GGCTGCAGGG CTGCCTGGCT
      A V F V T Q E E A H G V L H R R R R A N
61  GCCGTCTTCG TCACCCAGGA GGAAGCCCAT GGCGTCCTGC ATCGCCGGCG CCGGGCCAAT
      A F L E E L R P G S L E R E C K E E Q C
121  GCCTTTCTGG AAGAGCTCCG CCCTGGCTCC CTGGAACGCG AATGCAAAGA GGAACAGTGC
      S F E E A R E I F K D A E R T K L F W I
181  AGCTTTGAGG AAGCCCGGGA GATTTTCAAA GACGCTGAGC GGACCAAAC TTTTGGATT
      S Y S D G D Q C A S S P C Q N G G S C K
241  AGCTATAGCG ATGGCGATCA GTGCGCCTCC AGCCCTTGCC AGAACGGGGG CTCTTGCAAA
      D Q L Q S Y I C F C L P A F E G R N C E
301  GACCAGCTGC AGAGCTATAT CTGCTTCTGC CTGCCTGCCT TTGAGGGGCG CAATTGCGAA
      T H K D D Q L I C V N E N G G C E Q Y C
361  ACCCATAAGG ATGACCAGCT GATTTGCGTC AACGAAAACG GGGGCTGCGA GCAGTACTGC
      S D H T G T K R S C R C H E G Y S L L A
421  AGCGATCACA CGGGCACGAA GCGGAGCTGC CGCTGCCACG AAGGCTATAG CCTCCTGGCT
      D G V S C T P T V E Y P C G K I P I L E
481  GACGGGGTGT CCTGCACGCC CACGGTGGA TACCTTGCG GGAAGATTCC CATTTAGAA
      K R N A S K P Q G R I V G G K V C P K G
541  AAGCGAACG CTAGCAAACC CCAGGGCCGG ATCGTCGGCG GGAAGGTCTG CCCTAAGGGG
      E C P W Q V L L L V N G A Q L C G G T L
601  GAGTGCCCTT GGCAGGTCCT GCTCCTGGTC AACGGGGCCC AGCTGTGCGG CGGGACCTC
      I N T I W V V S A A H C F D K I K N W R
661  ATCAATACCA TTTGGGTCGT GTCCGCCGCT CACTGCTTCG ATAAGATTAA GAATTGGCGG
      N L I A V L G E H D L S E H D G D E Q S
721  AACCTCATCG CTGTGCTCGG CGAACACGAT CTGTCCGAGC ATGACGGGGA CGAACAGTCC
      R Q V A Q V I I P S T Y V P G T T N H D
781  CGCCGGGTGG CTCAGGTCAT CATTCCCTCC ACCTATGTGC CTGGCACGAC CAATCACGAT
      I A L L R L H Q P V V L T D H V V P L C
841  ATCGCTCTGC TCCGCCTCCA CCAGCCCGTC GTGCTCACCG ATCACGTCGT GCCTCTGTGC
      L P E R T F S E R T L A F V R F S L V S
901  CTGCCTGAGC GGACCTTTAG CGAACGCACG CTGGCTTTTC TCCGCTTTAG CCTCGTGTCC
      G W G Q L L D R G A T A L E L M V L N V
961  GGCTGGGGCC AGCTGCTCGA CCGGGGCGCT ACCGCTCTCG AGCTGATGGT GCTCAACGTC
      P R L M T Q D C L Q Q S R K V G D S P N
1021  CCCCGGCTGA TGACCCAGGA CTGCCTGCAG CAGTCCCGCA AAGTGGGGGA CTCCCCCAAT
      I T E Y M F C A G Y S D G S K D S C K G
1081  ATCACGGAGT ATATGTTTTG CGCTGGCTAT AGCGATGGCT CCAAGGATAG CTGCAAGGGG
      D S G G P H A T H Y R G T W Y L T G I V
1141  GACTCCGGCG GGCCCATGC CACGCACTAT CGCGGGACCT GGTACCTCAC CGGGATCGTC
      S W G Q G C A T V G H F G V Y T R V S Q
1201  AGCTGGGGCC AGGGCTGCGC CACGGTGGGG CACTTTGGCG TCTACACGCG CGTCAGCCAG
      Y I E W L Q K L M R S E P R P G V L L R
1261  TACATTGAGT GGCTGCAGAA GCTCATGCGG AGCGAACCCC GGCCCGGGT GCTCCTGCGG
      A P F P * L E P T Y C D L A P P A G T T
1321  GCCCCTTTCC CTTAACTGGA ACCCACGTAC TGCGACCTCG CCCCTCCCGC TGGCACGACC
      D A A H P G R S V V P A L L P L L A G T
1381  GATGCCGCTC ACCCTGGCCG GAGCGTCGTG CCTGCCCTCC TGCTCTGTCT CGCCGGGACC
      L L L L E T A T A P * * * *
1441  CTCTGTCTCC TGGAAACCGC TACCGCTCCC TAGTAATAGT GA

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Figure 18 (IFN-UGAG)

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      M A L P F A L L M A L V V L S C K S I C
1  ATGGCTTTGC CTTTGTGCTT ACTGATGGCC CTGGTGGTGC TCAGCTGCAA GTCCATATGC
      S L G C D L P Q T H S L G N R R A L I L
61 TCTCTAGGCT GTGATCTGCC TCAGACCCAC AGCCTGGGTA ATAGGAGGGC CTTGATACTC
      L A Q M G R I S P F S C L K D R H D F G
121 CTGGCACAAA TGGGAAGAAT CTCTCCTTTC TCCTGCCTGA AGGACAGACA TGACTTTTGA
      F P Q E E F D G N Q F Q K A Q A I S V L
181 TTCCCCCAGG AGGAGTTTGA TGGCAACCAG TTCCAGAAGG CTCAAGCCAT CTCTGTCTTC
      H E M I Q Q T F N L F S T K D S S A T W
241 CATGAGATGA TCCAGCAGAC CTTCAATCTC TTCAGCACAA AGGACTCATC TGCTACTTGG
      E Q S L L E K F S T E L N Q Q L N D L E
301 GAACAGAGCC TCCTAGAAAA ATTTTCCACT GAACTTAACC AGCAGCTGAA TGACCTGGAA
      A C V I Q E V G V E E T P L M N V D S I
361 GCCTGCGTGA TACAGGAGGT TGGGGTGGAA GAGACTCCCC TGATGAATGT GGACTCCATC
      L A V K K Y F Q R I T L Y L T E K K Y S
421 CTGGCTGTGA AGAAATACTT CCAAAGAATC ACTCTTTATC TGACAGAGAA GAAATACAGC
      P C A W E V V R A E I M R S F S L S K I
481 CCTTGTGCCT GGGAGGTTGT CAGAGCAGAA ATCATGAGAT CCTTCTCTTT ATCAAAAATT
      F Q E R L R R K E A A A G A P V P Y P D
541 TTTCAAGAAA GATTAAGGAG GAAGGAAGCG GCCGCA GGTG CGCCGGTGCC GTATCCGGAC
      P L E P R K E T A A A K F E R Q H M D S
601 CCGCTGGAAC CGCGTAAAGA AACCGCTGCT GCTAAATTCTG AACGCCAGCA CATGGACAGC
      * G K P I P N P L L G L D S T L E P T Y
661 TGAGGTAAGC CTATCCCTAA CCCTCTCCTC GGTCTCGATT CTACGCTGGA ACCCACGTAC
      C D L A P P A G T T D A A H P G R S V V
721 TGCGACCTCG CCCCTCCCGC TGGCAGGACC GATGCCGCTC ACCCTGGCCG GAGCGTCGTG
      P A L L P L L A G T L L L L E T A T A P
781 CCTGCCCTCC TGCCTCTGCT CGCCGGGACC CTCCTGCTCC TGGAAACCGC TACCGCTCCC
      * * * *
841 TAGTAATAGT GA

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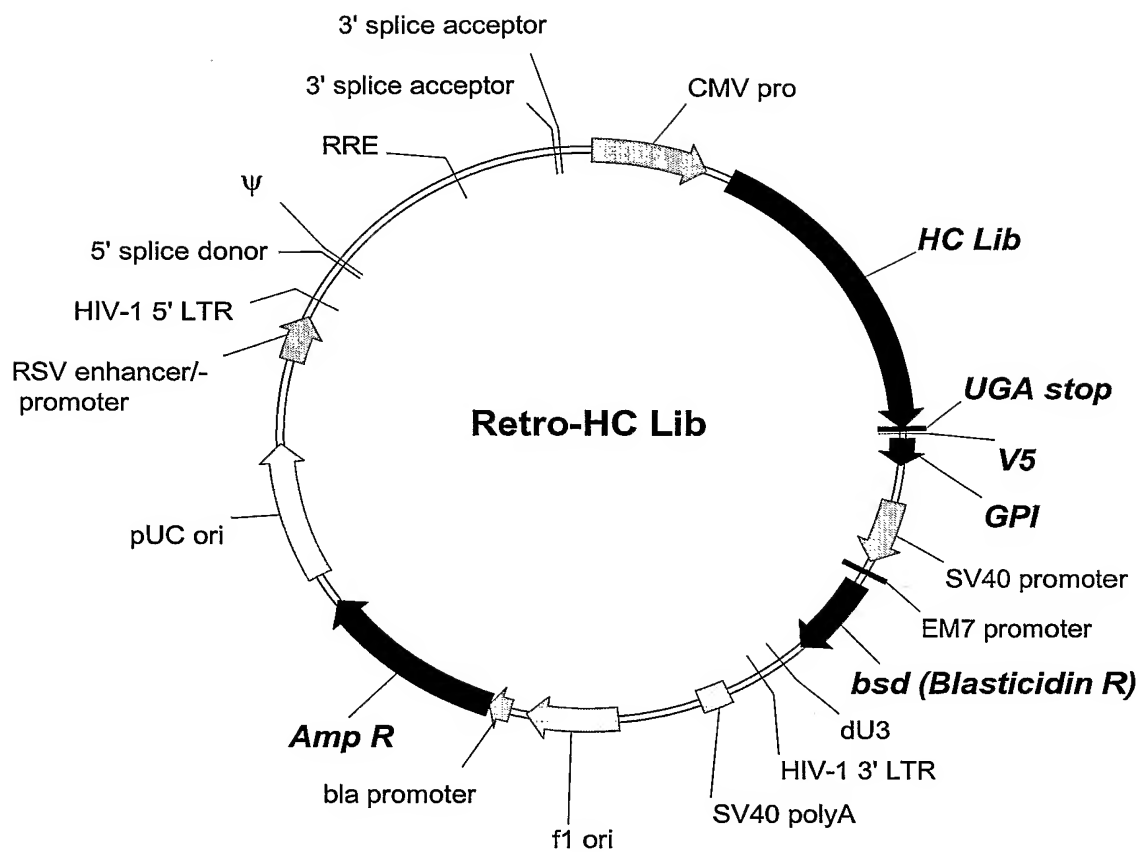
Figure 19

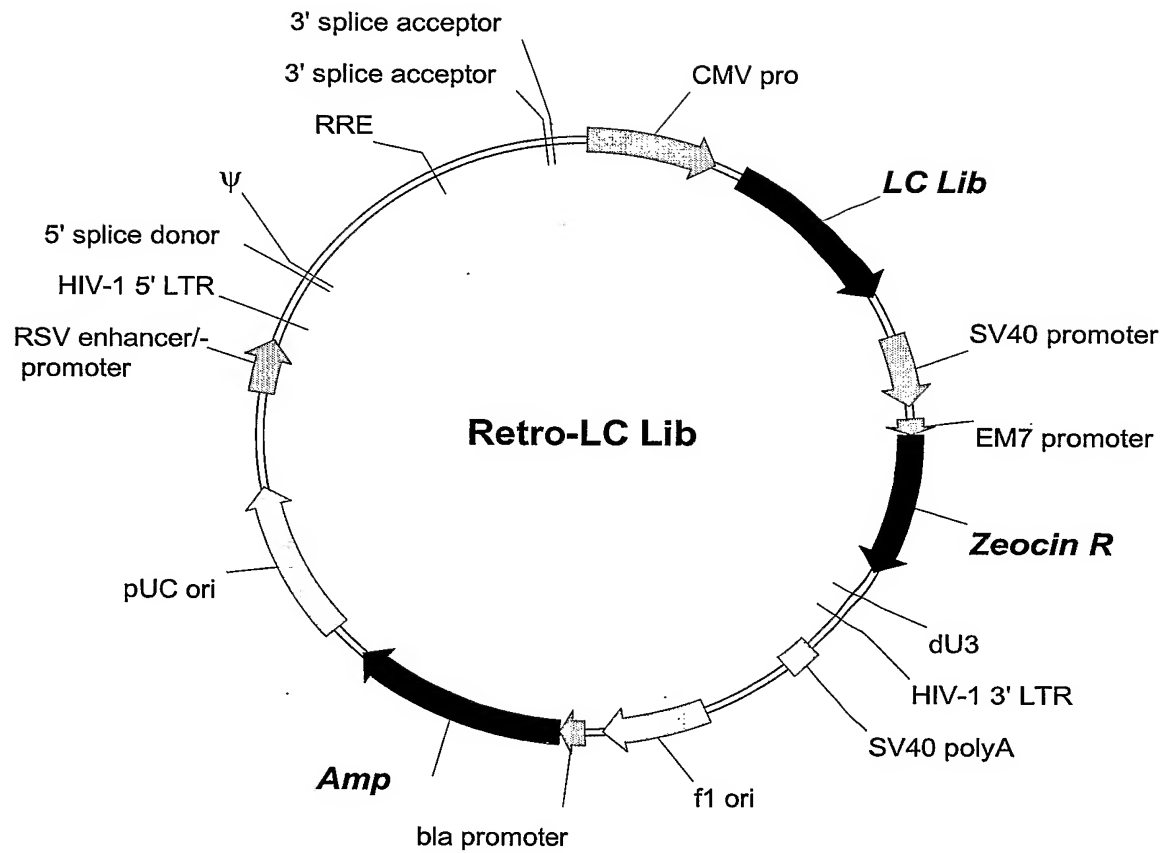
Figure 20

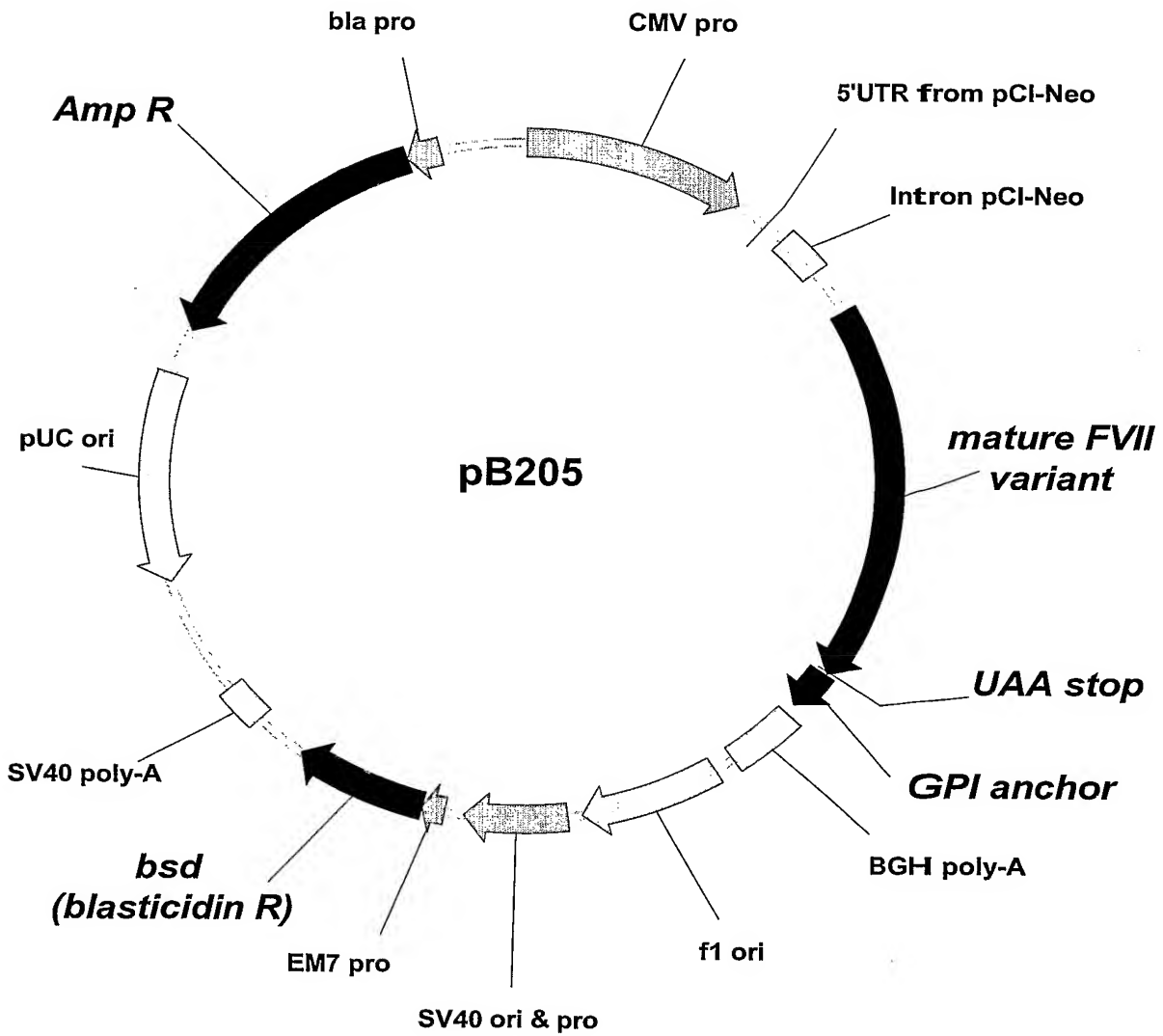
Figure 21

Figure 22 (FVII variant-UAA-GPI)

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      M V S Q   A L R   L L C   L L L G   L Q G   C L A
1  ATGGTCAGCC AGGCCCTCCG CCTCCTGTGC CTGCTCCTGG GGCTGCAGGG CTGCCTGGCT
      A V F V   T Q E   E A H   G V L H   R R R   R A N
61  GCCGTCTTCG TCACCCAGGA GGAAGCCCAT GGCGTCCTGC ATCGCCGGCG CCGGGCCAAT
      A F L E   E L R   Q G S   L E R E   C K E   E Q C
121  GCCTTTCTGG AAGAGCTCCG CCAGGGCTCC CTGGAACGCG AATGCAAAGA GGAACAGTGC
      S F E E   A R E   I F E   D E E E   T K L   F W I
181  AGCTTTGAGG AAGCCCGCGA GATTTTCGAA GACGAAGAAG AAACCAAGCT GTTTTGATT
      S Y S D   G D Q   C A S   S P C Q   N G G   S C K
241  AGCTATAGCG ATGGCGATCA GTGCGCCTCC AGCCCTTGCC AGAACGGGGG CTCCTGCAAA
      D Q L Q   S Y I   C F C   L P A F   E G R   N C E
301  GACCAGCTGC AGAGCTATAT CTGCTTCTGC CTGCTGCCT TTGAGGGGCG CAATTGCGAA
      T H K D   D Q L   I C V   N E N G   G C E   Q Y C
361  ACCCATAAGG ATGACCAGCT GATTTCGCTC AACGAAAACG GGGGCTGCGA GCAGTACTGC
      S D H N   G T K   R S C   R C H E   G Y S   L L A
421  AGCGATCACA ACGGCACGAA GCGGAGCTGC CGCTGCCACG AAGGCTATAG CCTCCTGGCT
      D G V S   C T P   T V E   Y P C G   K I P   I L E
481  GACGGGGTGT CCTGCACGCC CACGGTGGA TACCCTTGCG GGAAGATTCC CATTCTAGAA
      K R N A   S K P   Q G R   I V G G   K V C   P K G
541  AAGCGGAACG CCAGCAAACC CCAGGGCCGG ATCGTCGGCG GGAAGGTCTG CCCTAAGGGG
      E C P W   Q V L   L L V   N G A Q   L C G   G T L
601  GAGTGCCCCT GGCAGGTCCT GCTCCTGGTC AACGGGGCCC AGCTGTGCGG CGGGACCCTC
      I N T I   W V V   S A A   H C F D   K I K   N W R
661  ATCAATACCA TTTGGGTCGT GTCCGCGCT CACTGCTTCG ATAAGATTAA GAATTGGCGG
      N L I A   V L G   E H D   L S E H   D G D   E Q S
721  AACCTCATCG CTGTGCTCGG CGAACACGAT CTGTCCGAGC ATGACGGGGA CGAACAGTCC
      R R V A   Q V I   I P S   T Y V P   G T T   N H D
781  CGCCGGGTGG CTCAGGTCAT CATTCCCTCC ACCTATGTGC CTGGCACGAC CAATCACGAT
      I A L L   R L H   Q P V   N L T D   H V V   P L C
841  ATCGCTCTGC TCCGCCTCCA CCAGCCCGTC AACCTCACCG ATCACGTCGT GCCTCTGTGC
      L P E R   T F S   E R T   L A F V   R F S   L V S
901  CTGCCTGAGC GGACCTTTAG CGAACGCAG CTGGCTTTTCG TCCGCTTTAG CCTCGTGTCC
      G W G Q   L L D   R G A   T A L E   L M V   L N V
961  GGCTGGGGCC AGCTGCTCGA CCGGGGCGCT ACCGCTCTCG AGCTGATGGT GCTCAACGTC
      P R L M   T Q D   C L Q   Q S R K   V G D   S P N
1021  CCCC GGCTGA TGACCCAGGA CTGCCTGCAG CAGTCCCGCA AAGTGGGGGA CTCCCCAAT
      I T E Y   M F C   A G Y   S D G S   K D S   C K G
1081  ATCACGGAGT ATATGTTTTG CGCTGGCTAT AGCGATGGCT CCAAGGATAG CTGCAAGGGG
      D S G G   P H A   T H Y   R G T W   Y L T   G I V
1141  GACTCCGGCG GGCCCCATGC CACGCACTAT CGCGGGACCT GGTACCTCAC CGGGATCGTC
      S W G Q   G C A   T V G   H F G V   Y T R   V S Q
1201  AGTGGGGGCC AGGGCTGCGC CACGGTGGGG CACTTTGGCG TCTACACGCG CGTCAGCCAG
      Y I E W   L Q K   L M R   S E P R   P G V   L L R
1261  TACATTGAGT GGCTGCAGAA GCTCATGCGG AGCGAACCCC GGCCCGGGGT GCTCCTGCGG
      A P F P   * L E   P T Y   C D L A   P P A   G T T
1321  GCCCCTTTCC CTAACTGGA ACCCACGTAC TGCGACCTCG CCCCTCCCGC TGGCACGACC
      D A A H   P G R   S V V   P A L L   P L L   A G T
1381  GATGCCGCTC ACCCTGGCCG GAGCGTCGTG CCTGCCCTCC TGCCTCTGCT CGCCGGGACC
      L L L L   E T A   T A P   * * * *
1441  CTCCTGCTCC TGGAAACCGC TACCGCTCCC TAGTAATAGT GA

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Figure 23

